

Query Match 36.4%; Score 82; DB 4; Length 154;
Best local similarity 41.0%; Pred. No. 0.0057; DB 4;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

QY 2 EDPQRYYECCQECRQEEEROPQCQCRCLRFEQQQ 40
SEQUENCE FROM N.A.
MEDLINE=9250691; PubMed=1641350;
RA Hashimoto S., Fujita H., Hasegawa S., Roeder R.G., Horikoshi M.;
RT Conserved structural motifs within the N-terminal domain of TFIID tau
From Xenopus, mouse and human.";
RL Nucleic Acids Res. 20:3788-3789(1992).
SEQUENCE 154 AA; 16790 MW; 93A5A0B5CCAF604 CRC64;

RESULT 10
016845 PRELIMINARY; PRT; 339 AA.
AC 016845;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE SEQUENCE-BINDING PROTEIN (TATA-BOX FACTOR) (TATA
Homo sapiens (Human)).
OS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
ID Soderblom F., Anand C., Iranfar N., Loomis W.P.;
RT "An adenylyl cyclase that functions during late development of
Dictyostelium.";
DR Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF153562; RAD50121.1; -.
DR HSSP; P19754; IAKW.
DR INTERPRO; IPR00410; -.
DR INTERPRO; IPR0054; -.
DR INTERPRO; IPR00440; -.
DR INTERPRO; IPR00596; -.
DR INTERPRO; IPR00789; -.
DR PFAM; PF00072; response_reg; 1.
DR PFAM; PF00211; quanylate_cyc; 1.
DR PRINTS; PR00344; BCTRISENSOR.
DR PROSITE; PS00387; PPASE; UNKNOWN_1.
SQ SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;

Query Match 36.2%; Score 81.5; DB 5; Length 2123;
Best Local Similarity 43.6%; Pred. No. 0.056; DB 5;
Matches 17; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

QY 2 EDPQRYYECCQECRQEEEROPQCQCRCLRFEQQQ 40
SEQUENCE FROM N.A.
MEDLINE=90302010; PubMed=2194289;
RA Kao C., Lieberman P., Schmidt M., Zhou Q., Pei R., Berk A.J.;
RT "Cloning of a transcriptionally active human TATA binding factor.";
RL Science 248:1626-1630(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=FBROBLAST;
ID Kao C., Lieberman P., Schmidt M., Zhou Q., Pei R., Berk A.J.;
RL Submitted (JUN-1990) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
THE POSITION OF TRANSCRIPTION INITIATION.
CC -!- SUBUNIT: BINDS DNA AS A MONOMER.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: THE C-TERMINAL 180 RESIDUES ARE EXTREMELY WELL
CONSERVED IN ALL EUKARYOTIC TFIID.
CC -!- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS.
DR EMBL; M34960; AAC03409.1; -.
DR P20226; ITGBH.
DR INTERPRO; IPR00814; -.
DR PFAM; PF00352; TBP; 2.
DR PRINTS; PR00686; TIEFACTORID.
DR PROSITE; PS00351; TFIID; 2.
RW transcription regulation; DNA-binding; Nuclear protein; Duplication.
SQ SEQUENCE 339 AA; 37783 MW; 98B7E26C84B853a CRC64;

Query Match 36.4%; Score 82; DB 4; Length 339;
Best Local Similarity 41.0%; Pred. No. 0.011; DB 4;
Matches 16; Conservative 14; Mismatches 9; Indels 0; Gaps 0;

RESULT 11
090957 PRELIMINARY; PRT; 2123 AA.
ID Q9U957
AC 09U957;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE ADENYLYL CYCLASE.
GN ACRA.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX4;
ID Soderblom F., Anand C., Iranfar N., Loomis W.P.;
RT "An adenylyl cyclase that functions during late development of
Dictyostelium.";
DR Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF153562; RAD50121.1; -.
DR HSSP; P19754; IAKW.
DR INTERPRO; IPR00410; -.
DR INTERPRO; IPR0054; -.
DR INTERPRO; IPR00440; -.
DR INTERPRO; IPR00596; -.
DR INTERPRO; IPR00789; -.
DR PFAM; PF00072; response_reg; 1.
DR PFAM; PF00211; quanylate_cyc; 1.
DR PRINTS; PR00344; BCTRISENSOR.
DR PROSITE; PS00387; PPASE; UNKNOWN_1.
SQ SEQUENCE 2123 AA; 243039 MW; 744247140BC342FA CRC64;

Query Match 36.2%; Score 81.5; DB 5; Length 2123;
Best Local Similarity 43.6%; Pred. No. 0.056; DB 5;
Matches 17; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

QY 2 EDPQRYYECCQECRQEEEROPQCQCRCLRFEQQQ 40
SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Gocayne J.D.,
RA Ananatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champé M., Peiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heijt G., Nelson C.R., Miklos G.I.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

us-09-331-631a-8_copy_80_119.rspt

RESULT	15
ID	04011
AC	044011;
DT	01-JUN-1998 (TREMBLrel. 06, Created)
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	PROTEIN KINASE YAKA.
GN	YAKA.
OS	Dictyostelium discoideum (Slime mold).
OC	Eukaryota; Dictyostelliida; Dictyostelium.
OX	NCBI TaxID:44689;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=AK800;
RX	MEDLINE=96042901; PubMed=8536963;
RA	Loomis W.F., Walker D., Hughes J., Maghakian D., Kuspa A.;
RT	"Integrated maps of the chromosomes in Dictyostelium discoideum Genetics 141:147-157(1995)."
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=AK800;
RX	MEDLINE=96224325; PubMed=8643615;
RA	Kuspa A., Loomis W.F.;
RT	"Ordered yeast artificial chromosome clones representing the Dictyostelium discoideum genome";
RT	Proc. Natl. Acad. Sci. U.S.A. 93:5562-5566(1996)."
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=AK800;
RA	Kuspa A., Lu S., Souza G.M.;
RL	Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AF045453; AAC02554.1; -.
DR	HSSP; P24941; ICKP.
DR	INTERPRO; IPR00719; -.
DR	INTERPRO; IPR02290; -.
DR	PFAM; PF00059; -.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
SQ	SEQUENCE 1457 AA; 167110 MW; C1FC0CE99D5618556 CRC64;

Query Match Similarity 35.6%; Score 80; DB 5; Length 1457;
 Best Local Match 38.5%; Fred. No. 0.062; Mismatches 10; Indels 0; Gaps 0
 Matches 15; Conservative 14; Mismatches 10; Indels 0; Gaps 0

Search completed: March 1, 2001, 16:09:34
Job time: 1578 sec